RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/797,248_

Source _IFWO_

Date Processed by STIC: _3/22/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 10/08/03

IFWO

RAW SEQUENCE LISTING   DATE: 03/22/2004
PATENT APPLICATION: US/10/797,248   TIME: 09:34:26

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\03222004\J797248.raw

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 3 <110> APPLICANT: Dumas, Renaud
 4         Lebrun, Marc-Henri
 5         Zundel, Jean-Luc
 6         Effantin, G,raldine
 7         Morin, Val,rie
 9 <120> TITLE OF INVENTION: Use of inhibitors of ketol-acid reductoisomerase to prevent
or treat
10         fungal infection of plants
12 <130> FILE REFERENCE: A36156-PCT-USA-A 072667.0196
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/797,248
C--> 15 <141> CURRENT FILING DATE: 2004-03-10
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: Custom
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 402
23 <212> TYPE: PRT
24 <213> ORGANISM: Magnaporthe grisea
26 <220> FEATURE:
27 <221> NAME/KEY: TRANSIT
28 <222> LOCATION: (1)..(51)
29 <223> OTHER INFORMATION: Putative mitochondrial transit peptide
31 <400> SEQUENCE: 1
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36              20                  25                  30
38 Met Val Arg Ala Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln
39          35                  40                  45
41 Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
42      50                  55                  60
44 Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
45  65                  70                  75                  80
47 Asp Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln
48              85                  90                  95
50 Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg
51             100                 105                 110
53 Lys Asp Gly Lys Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro
54             115                 120                 125
56 Gly Lys Asn Leu Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val
57         130                 135                 140
59 Ile Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala
60 145                 150                 155                 160
62 Leu Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly
63             165                 170                 175
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65 Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp
66             180                 185                 190
68 Val Asp Val Ile Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg
69             195                 200                 205
71 Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr
72     210                 215                 220
74 Gln Asp Val Thr Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val
75 225                 230                 235                 240
77 Ala Ile Gly Ser Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val
78             245                 250                 255
80 Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His
81             260                 265                 270
83 Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser
84             275                 280                 285
86 Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu·
87     290                 295                 300
89 Tyr Pro Leu Ile Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys
90 305                 310                 315                 320
92 Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys
93             325                 330                 335
95 Asp Ala Leu Lys Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp
96             340                 345                 350
98 Gly Ser Glu Thr Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr
99             355                 360                 365
101 Arg Glu Lys Tyr Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile
102     370                 375                 380
104 Trp Arg Ala Gly Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
105 385                 390                 395                 400
107 Gln Lys
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 395
113 <212> TYPE: PRT
114 <213> ORGANISM: Saccharomyces cerevisiae
116 <220> FEATURE:
117 <221> NAME/KEY: TRANSIT
118 <222> LOCATION: (1)..(47)
119 <223> OTHER INFORMATION: mitochondrial transit peptide
121 <300> PUBLICATION INFORMATION:
122 <308> DATABASE ACCESSION NO: gb:X04969
123 <309> DATABASE ENTRY DATE: 1993-09-12
125 <400> SEQUENCE: 2
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131             20                  25                  30
133 Arg Pro Ala Ala Arg Phe Val Lys Pro Met Ile Thr Thr Arg Gly Leu
134             35                  40                  45
136 Lys Gln Ile Asn Phe Gly Gly Thr Val Glu Thr Val Tyr Glu Arg Ala
137     50                  55                  60
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139 Asp Trp Pro Arg Glu Lys Leu Leu Asp Tyr Phe Lys Asn Asp Thr Phe
140  65               70               75               80
142 Ala Leu Ile Gly Tyr Gly Ser Gln Gly Tyr Gly Gln Gly Leu Asn Leu
143               85               90               95
145 Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Ala
146              100              105              110
148 Ser Trp Lys Ala Ala Ile Glu Asp Gly Trp Val Pro Gly Lys Asn Leu
149              115              120              125
151 Phe Thr Val Glu Asp Ala Ile Lys Arg Gly Ser Tyr Val Met Asn Leu
152      130              135              140
154 Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Ile Lys Pro Leu
155 145              150              155              160
157 Leu Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
158              165              170              175
160 Phe Lys Asp Leu Thr His Val Glu Pro Pro Lys Asp Leu Asp Val Ile
161              180              185              190
163 Leu Val Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Lys
164              195              200              205
166 Glu Gly Arg Gly Ile Asn Ser Ser Tyr Ala Val Trp Asn Asp Val Thr
167      210              215              220
169 Gly Lys Ala His Glu Lys Ala Gln Ala Leu Ala Val Ala Ile Gly Ser
170 225              230              235              240
172 Gly Tyr Val Tyr Gln Thr Thr Phe Glu Arg Glu Val Asn Ser Asp Leu
173              245              250              255
175 Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
176              260              265              270
178 Ala Gln Tyr Asp Val Leu Arg Glu Asn Gly His Ser Pro Ser Glu Ala
179          275              280              285
181 Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile
182          290              295              300
184 Gly Lys Tyr Gly Met Asp Tyr Met Tyr Asp Ala Cys Ser Thr Thr Ala
185 305              310              315              320
187 Arg Arg Gly Ala Leu Asp Trp Tyr Pro Ile Phe Lys Asn Ala Leu Lys
188              325              330              335
190 Pro Val Phe Gln Asp Leu Tyr Glu Ser Thr Lys Asn Gly Thr Glu Thr
191              340              345              350
193 Lys Arg Ser Leu Glu Phe Asn Ser Gln Pro Asp Tyr Arg Glu Lys Leu
194              355              360              365
196 Glu Lys Glu Leu Asp Thr Ile Arg Asn Met Glu Ile Trp Lys Val Gly
197      370              375              380
199 Lys Glu Val Arg Lys Leu Arg Pro Glu Asn Gln
200 385              390              395
203 <210> SEQ ID NO: 3
204 <211> LENGTH: 400
205 <212> TYPE: PRT
206 <213> ORGANISM: Neurospora crassa
208 <220> FEATURE:
209 <221> NAME/KEY: TRANSIT
210 <222> LOCATION: (1)..(53)
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RAW SEQUENCE LISTING   DATE: 03/22/2004
PATENT APPLICATION: US/10/797,248   TIME: 09:34:26

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\03222004\J797248.raw

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211 <223> OTHER INFORMATION: putative mitochondrial transit peptide
213 <300> PUBLICATION INFORMATION:
214 <308> DATABASE ACCESSION NO: gb:M84189.1
215 <309> DATABASE ENTRY DATE: 1996-05-23
217 <400> SEQUENCE: 3
218 Met Ala Ala Arg Asn Cys Thr Lys Ala Leu Arg Pro Leu Ala Arg Gln
219  1               5                  10                  15
221 Leu Ala Thr Pro Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ala Ser
222              20                  25                  30
224 Ala Val Arg Ala Ser Val Ala Val Lys Ala Val Ala Ala Pro Ala Arg
225          35                  40                  45
227 Gln Gln Val Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu
228      50                  55                  60
230 Glu Val His Glu Arg Ala Asp Trp Pro Ala Glu Lys Leu Leu Asp Tyr
231 65                  70                  75                  80
233 Phe Lys Asn Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His
234                  85                  90                  95
236 Gly Gln Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Val Gly
237              100                 105                 110
239 Val Arg Lys Asn Gly Lys Ser Trp Glu Asp Ala Ile Gln Asp Gly Trp
240          115                 120                 125
242 Val Pro Gly Lys Asn Leu Phe Asp Val Asp Glu Ala Ile Ser Arg Gly
243      130                 135                 140
245 Thr Ile Val Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp
246 145                 150                 155                 160
248 Pro His Ile Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser
249                  165                 170                 175
251 His Gly Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro
252              180                 185                 190
254 Thr Asp Val Asp Val Ile Leu Val Ala Pro Lys Gly Ser Gly Arg Thr
255          195                 200                 205
257 Val Arg Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala
258      210                 215                 220
260 Val Tyr Gln Asp Val Thr Gly Lys Ala Lys Glu Lys Ala Val Ala Leu
261 225                 230                 235                 240
263 Gly Val Ala Val Gly Ser Gly Tyr Leu Tyr Glu Thr Thr Phe Glu Lys
264              245                 250                 255
266 Glu Val Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly
267              260                 265                 270
269 Ile His Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly
270          275                 280                 285
272 His Ser Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln
273      290                 295                 300
275 Ser Leu Tyr Pro Leu Ile Gly Ala His Gly Met Asp Trp Met Phe Asp
276 305              310                 315                 320
278 Ala Cys Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Thr Pro Lys
279              325                 330                 335
281 Phe Lys Asp Ala Leu Lys Pro Val Phe Asn Asn Leu Tyr Asp Ser Val
282          340                 345                 350
```

```
284 Lys Asn Gly Asp Glu Arg Lys Arg Ser Leu Glu Tyr Asn Ser Gln Pro
285         355                 360                 365
287 Asp Tyr Arg Glu Arg Tyr Glu Ala Glu Leu Asp Glu Ile Arg Asn Leu
288         370                 375                 380
290 Glu Ile Trp Arg Ala Gly Lys Arg Ser Leu Arg Pro Glu Asn Gln Lys
291 385                 390                 395                 400
297 <210> SEQ ID NO: 4
298 <211> LENGTH: 1356
299 <212> TYPE: DNA
300 <213> ORGANISM: Magnaporthe grisea
302 <220> FEATURE:
303 <221> NAME/KEY: 5'UTR
304 <222> LOCATION: (1)..(43)
306 <220> FEATURE:
307 <221> NAME/KEY: CDS
308 <222> LOCATION: (44)..(1246)
310 <220> FEATURE:
311 <221> NAME/KEY: 3'UTR
312 <222> LOCATION: (1247)..(1356)
314 <220> FEATURE:
315 <221> NAME/KEY: polyA_site
316 <222> LOCATION: (1322)..(1330)
318 <400> SEQUENCE: 4
319 ttgtttttct tggttcctta ttctaccttg tcacacaaca aac atg tct gct cgc     55
320                                                 Met Ser Ala Arg
321                                                 1
323 ggt ttc tca aag gct ttg agg cca atg gcc cgc caa ttg gcc act ccc    103
324 Gly Phe Ser Lys Ala Leu Arg Pro Met Ala Arg Gln Leu Ala Thr Pro
325   5                 10                  15                  20
327 gcc gtt cag agg cgt acc ttc gtg gct gct tct agc atg gtg cgg gcc    151
328 Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ser Ser Met Val Arg Ala
329                 25                  30                  35
331 acc agg aaa gcc gcc gtc gct ccc act cag cag cag atc cgt ggt gtc    199
332 Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln Ile Arg Gly Val
333             40                  45                  50
335 aag acc atg gat ttt gct ggc cac aag gag cag gtc tgg gag cgt gcc    247
336 Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val Trp Glu Arg Ala
337         55                  60  .                65
339 gac tgg ccc aag gag aag ctg ctg gag tac ttc aag gac gac acc ctt    295
340 Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys Asp Asp Thr Leu
341     70                  75                  80
343 gcc ctc atc ggc tat ggt tcg cag ggc cac ggc cag ggt ctt aac ctc    343
344 Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln Gly Leu Asn Leu
345 85                  90                  95                  100
347 cgc gac aac ggc ctc aac gtc atc atc ggt gtg cgc aag gac gga aag    391
348 Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Lys
349                 105                 110                 115
351 tcg tgg aag gac gcc gtc cag gac ggc tgg gtt ccc ggc aag aac ctc    439
352 Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro Gly Lys Asn Leu
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/22/2004
PATENT APPLICATION: **US/10/797,248**   TIME: 09:34:27

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03222004\J797248.raw**

Please **Note:**
Use of **n** and/or **Xaa** have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 9,12
Seq#:9; N Pos. 6,12,15,18
Seq#:10; N Pos. 6,9,18

VARIABLE LOCATION SUMMARY   DATE: 03/22/2004
PATENT APPLICATION: **US/10/797,248**   TIME: 09:34:27

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03222004\J797248.raw**

Use of n's or Xaa's(NEW RULES): *Error Explanation:* ℛ
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:8; N Pos. 9,12
Seq#:9; N Pos. 6,12,15,18
Seq#:10; N Pos. 6,9,18

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<210> SEQ ID NO 8
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence: primer 2
<400> SEQUENCE: 8
      atgttyyrng dncartayga                                          20

<210> SEQ ID NO 9
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence: primer 3
<400> SEQUENCE: 9
      gaygdntggg tncdnggnaa                                          20

<210> SEQ ID NO 10
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence: primer 4
<400> SEQUENCE: 10
      atggdnggna tacayggnat g                                        21
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[Handwritten annotations:]

please explain "N" locations and which location "N" Represents.

← please explain, same error

← please explain, same error

(Please see error explanation on page 7.)

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/797,248**

DATE: 03/22/2004
TIME: 09:34:27

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03222004\J797248.raw**

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:609 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8
L:609 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:621 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9
L:621 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:633 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10
L:633 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10
L:633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0